



2/12/02

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/056,454
Source: OLPE
Date Processed by STIC: 2/15/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/056,454

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ✓ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPF

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/056,454

DATE: 02/15/2002
TIME: 14:39:23

Input Set : A:\EP.txt
Output Set: N:\CRF3\02152002\J056454.raw

Does Not Comp
Corrected Diskette Reader

SEQUENCE LISTING

see p. 20

4 (1) GENERAL INFORMATION:
E--> 6 (i) APPLICANT:
15 (ii) TITLE OF INVENTION: Improvements in or Relating to Plant Starch
16 Composition
18 (iii) NUMBER OF SEQUENCES: 20
E--> 0 (iv) CORRESPONDENCE ADDRESS:
9 (B) STREET: 501 Silverside Road, Suite 27
10 (C) CITY: Wilmington
11 (D) STATE: Delaware
12 (E) COUNTRY: United States of America
C--> 13 (F) ZIP: 19809
C--> 20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
C--> 0 (vi) CURRENT APPLICATION DATA:
C--> 0 (A) APPLICATION NUMBER: US/10/056,454
C--> 0 (B) FILING DATE: 24-Jan-2002
C--> 0 (viii) ATTORNEY/AGENT INFORMATION:
7 (A) NAME: National Starch and Chemical Investment
8 Holding Corporation

also,
see item 4
on Encl
Summary Sheet

ERRORED SEQUENCES

27 (2) INFORMATION FOR SEQ ID NO: 1:
29 (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 57 base pairs
31 (B) TYPE: nucleic acid
32 (C) STRANDEDNESS: single
33 (D) TOPOLOGY: linear
39 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
E--> 41 AAGGATCCGT CGACATCGAT AATACGACTC ACTATAGGGA TTTT
42 TTTT 57
204 (2) INFORMATION FOR SEQ ID NO: 12:
206 (i) SEQUENCE CHARACTERISTICS:
207 (A) LENGTH: 3003 base pairs
208 (B) TYPE: nucleic acid
209 (C) STRANDEDNESS: single
210 (D) TOPOLOGY: linear
216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

global format error

57

RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/056,454

TIME: 14:39:24

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Output Set: N:\CRF3\02152002\J056454.raw

E--> 218 GATGGGGCCT TGAAGTACAG AATTTGACAC TCAGTTAGTT ACACCTGCCAT
 219 CACTTATCAG 60

E--> 221 ATCTCTATTT TTTCTCTTAA TTCCAACCAA GGAATGAATA AAAAGATAGA
 222 TTTGTAAAAA 120

E--> 224 CCCTAAGGAG AGAAGAAGAA AGATGGTGTA TACACTCTCT GGAGTTCGTT
 225 TTCCTACTGT 180

E--> 227 TCCATCAGTG TACAAATCTA ATGGATTCAG CAGTAATGGT GATCGGAGGA
 228 ATGCTAATAT 240

E--> 230 TTCTGTATTC TTGAAAAAAC ACTCTCTTTC ACGGAAGATC TTGGCTGAAA
 231 AGTCTTCTTA 300

E--> 233 CAATTCCGAA TCCCGACCTT CTACAATTGC AGCATCGGGG AAAGTCCTTG
 234 TGCCTGGAAT 360

E--> 236 CCAGAGTGAT AGCTCCTCAT CCTCAACAGA TCAATTGAG TTCGCTGAGA
 237 CATCTCCAGA 420

E--> 239 AAATTCCTCA GCATCAACTG ATGTAGATAG TTCAACAATG GAACACGCTA
 240 GCCAGATTAA 480

E--> 242 AACTGAGAAC GATGACGTTG AGCCGTC AAG TGATCTTACA
 243 GGAAGTGTTG AAGAGCTGGA 540

E--> 245 TTTTGCTTCA TCACTACAAC TACAAGAAGG TGGTAACTG GAGGAGTCTA
 246 AAACATTAAA 600

E--> 248 TACTTCTGAA GAGACAATTA TTGATGAATC TGATAGGATC AGAGAGAGGG
 249 GCATCCCTCC 660

E--> 251 ACCTGGACTT GGTGAGAAGA TTTATGAAAT AGACCCCTTT TTGACAAACT
 252 ATCGTCAACA 720

E--> 254 CTTTGATTAC AGGTATTAC AGTACAAGAA ACTGAGGGAG GCAATTGACA
 255 AGTATGAGGG 780

E--> 257 TGGTTTGAA GCTTTTCTC GTGGTTATGA AAGAATGGGT TTCACTCGTA
 258 GTGCTACAGG 840

E--> 260 TATCACTTAC CGTGAGTGGG CTCCTGGTGC CCAGTCAGCT
 261 GCCCTCATTG GGGATTTC A 900

E--> 263 CAATGGGAC GCAAATGCTG ACTTTATGAC TCGGAATGAA TTTGGTGTCT
 264 GAGAGATTTT 960

E--> 266 TCTGCCAAAT AATGTGGATG GTTCTCCTGC AATTCCTCAT GGGTCCAGAG
 267 TGAAGATACG 1020

E--> 269 TATGGACACT CCATCAGGTG TTAAGGATTC CATTCTGCT TGGATCAACT
 270 ACTCTTTACA 1080

E--> 272 GCTTCTGAT GAAATCCAT ATAATGGAAT ATATTATGAT CCACCCGAAG
 273 AGGAGAGGTA 1140

E--> 275 TATCTTCCAA CACCCACGGC CAAAGAAACC AAAGTCGGTG AGAATATATG
 276 AATCTCATAT 1200

E--> 278 TGGGAATGAGT AGTCCGGAGC CTAAAATTAA CTCATACGTG AATTTTAGAG
 279 ATGAAGTTCT 1260

E--> 281 TCCTCGCATA AAAAAAGCTT GGGTACAATG CGGTGCAAAAT TATGGCTATT
 282 CAAGAGCATT 1320

E--> 284 CTTATTATGC TAGTTTGGT TATCATGTCA CAAATTTTTT TGCACCAAGC
 285 AGCCGTTTTG 1380

E--> 287 GAACGCCCGA CGACCTTAAG TCTTTGATTG ATAAAGCTCA TGAGCTAGGA
 288 ATGTTGTTTC 1440

E--> 290 TCATGGACAT TGTTACAGC CATGCATCAA ATAATACTTT AGATGGACTG

name
enum

RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/056,454

TIME: 14:39:24

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Output Set: N:\CRF3\02152002\J056454.raw

291 AACATGTTTG 1500
E--> 293 ACGGCACAGA TAGTGTGTTAC TTCTACTCTG GAGCTCGTGG TTATCATTTGG
294 ATGTGGGATT 1560
E--> 296 TCCGCCTCTT TAACATATGGA AACTGGGAGG TACTTAGGTA TCTTCTCTCA
297 AATGCGAGAT 1620
E--> 299 GGTGGTTGGA TGAGTTCAAA TTTGATGGAT TTAGATTTGA TGGTGTGACA
300 TCAATGATGT 1680
E--> 302 GTACTCACCA CGGATTATCG GTGGGATTCA CTGGGAACATA
303 CGAGGAATAC TTTGGACTCG 1740
E--> 305 CAACTGATGT GGATGCTGTT GTGTATCTGA TGCTGGTCAA CGATCTTATT
306 CATGGGCTTT 1800
E--> 308 TCCCAGATGC AATTACCATT GGTGAAGATG TTAGCGGAAT GCCGACATTT
309 TGTGTTCCCG 1860
E--> 311 TTCAAGATGG GGGTGTGTCG TTTGACTATC GGCTGCATAT GGCAATTGCT
312 GATAAATGGA 1920
E--> 314 TTGAGTTGCT CAAGAAACGG GATGAGGATT GGAGAGTGGG
315 TGATATTGTT CATACACTGA 1980
E--> 317 CAAATAGAAG ATGGTCGGAA AAGTGTGTTT CATACGCTGA AAGTCATGAT
318 CAAGCTCTAG 2040
E--> 320 TCGGTGATAA AACTATAGCA TTCTGGCTGA TGGACAAGGA TATGTATGAT
321 TTTATGGCTC 2100
E--> 323 TGGATAGACC GTCAACATCA TTAATAGATC GTGGGATAGC ATTACACAAG
324 ATGATTAGGC 2160
E--> 326 TTGTAACAT GGGATTAGGA GGAGAAGGGT ACCTAAATTT CATGGGAAAT
327 GAATTCGGCC 2220
E--> 329 ACCCTGAGTG GATTGATTTC CCTAGGGCTG AACAAACACCT CTCTGATGGC
330 TCAGTAATTC 2280
E--> 332 CCAGAAACCA ATTCAGTTAT GATAAATGCA GACGGAGATT TGACCTGGGA
333 GATGCAGAAT 2340
E--> 335 ATTTAAGATA CCGTGGGTTG CAAGAATTTG ACCGGGCTAT GCAGTATCTT
336 GAAGATAAAT 2400
E--> 338 ATGAGTTTAT GACTTCAGAA CACCAGTTCA TATCACGAAA GGATGAAGGA
339 GATAGGATGA 2460
E--> 341 TTGTATTGTA AAAAGGAAAC CTAGTTTTTG TCTTTAATTT TCACCTGGACA
342 AAAGGCTATT 2520
E--> 344 CAGACTATCG CATAGGCTGC CTGAAGCCTG GAAAATACAA
345 GGTTCCTTGG GACTCAGATG 2580
E--> 347 ATCCACTTTT TGGTGGCTTC GGGAGAATTG ATCATAATGC CGAATATTTT
348 ACCTTTGAAG 2640
E--> 350 GATGGTATGA TGATCGTCTT CGTTCAATTA TGGTGTATGC ACCTAGTAGA
351 ACAGCAGTGG 2700
E--> 353 TCTATGCACT AGTAGACAAA GAAGAAGAAG AAGAAGAAGA AGTAGCAGTA
354 GTAGAAGAAG 2760
E--> 356 TAGTAGTAGA AGAAGAATGA ACGAACTTGT GATCGCGTTG AAAGATTTGA
357 ACGCCACATA 2820
E--> 359 GAGCTTCTTG ACGTATCTGG CAATATTGCA TTAGTCTTGG CGGAATTTCA
360 TGTGACAACA 2880
E--> 362 GGTGTGCAAT TCTTTCCACT ATTAGTAGTG CAACGATATA CGCAGAGATG
363 AAGTGCTGAA 2940

Done

RAW SEQUENCE LISTING

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Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

E--> 365 CAAAAACATA TGTAATAATCG ATGAATTTAT GTCGAATGCT GGGACGATCG
 366 AATTCCTGCA 3000
 368 GCC
 370 (2) INFORMATION FOR SEQ ID NO: 13:
 372 (i) SEQUENCE CHARACTERISTICS:
 373 (A) LENGTH: 2975 base pairs
 374 (B) TYPE: nucleic acid
 375 (C) STRANDEDNESS: single
 376 (D) TOPOLOGY: linear
 382 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

E--> 384 TTGATGGGCC TTGAATCAG CAATTGACA CTCAGTTAGT TACACTCCTA
 385 TCACTTATCA 60
 E--> 387 GATCTCTATT TTTTCTCTTA ATTCCAACCA GGGGAATGAA TAAAAGGATA
 388 GATTGTGAAA 120
 E--> 390 AACCCCTAAGG AGAGAAGAAG AAAGATGGTG TATATACTCT CTGGAGTTCCG
 391 TTTTCCTACT 180
 E--> 393 GTTCCATCAG TGTACAAATC TAATGGATTC AGCAGTAATG GTGATCGGAG
 394 GAATGCTAAT 240
 E--> 396 GTTCTGTAT TCTTGAAAA GCACCTCTCTT TCACGGAAGA TCTTGGCTGA
 397 AAAGTCTTCT 300
 E--> 399 TACAATTCCG AATTCGGACC TTCTACAGTT GCAGCATCGG GGAAAGTCCT
 400 TGTGCCTGGA 360
 E--> 402 ACCCAGAGTG ATAGCTCCTC ATCCTCAACA GACCAATTTG AGTTCACTGA
 403 GACATCTCCA 420
 E--> 405 GAAAATTCCT CAGCATCAAC TGATGTAGAT AGTTCAACAA TGGAAACACGC
 406 TAGCCAGATT 480
 E--> 408 AAAACTGAGA ACGATGACGT TGAGCCGTCA AGTGATCTTA
 409 CAGGAAGTGT TGAAGAGCTG 540
 E--> 411 GATTTTGCTT CATCACTACA ACTACAAGAA GGTGGTAAAC TGGAGGAGTC
 412 TAAACATTA 600
 E--> 414 AATACTTCTG AAGAGACAAT TATTGATGAA TCTGATAGGA TCAGAGAGAG
 415 GGGCATCCCT 660
 E--> 417 CCACCTGGAC TTGGTCAGAA GATTTATGAA ATAGACCCCC TTTTGACAAA
 418 CTATCGTCAA 720
 E--> 420 CACCTTGATT ACAGGTATTC ACAGTACAAG AAAGTGAGGG AGGCAATTGA
 421 CAAGTATGAG 780
 E--> 423 GGTGGTTTGG AAGCTTTTCT CGTGGTTATG AAAAAATGGG TTTCACCTCGT
 424 AGTGCTACAG 840
 E--> 426 GTATCACTTA CCGTGAGTGG GCTCCTGGTG CCCAGTCAGC
 427 TGCCCTCATT GGAGATTTC 900
 E--> 429 ACAATTGGGA CGCAAAATGCT GACATTATGA CTCGGAATGA ATTTGGTGTG
 430 TGGGAGATT 960
 E--> 432 TTCTGCCCCAAA TAATGTGGAT GGTTCCTCTG CAATTCCCTCA TGGGTCCAGA
 433 GTGAAGATAC 1020
 E--> 435 GTATGGACAC TCCATCAGGT GTTAAGGATT CCATTCCTGC TTGGATCAAC
 436 TACTCTTTAC 1080
 E--> 438 AGCTTCCTGA TGAAATTCCA TATAATGGAA TATATTATGA TCCACCCGAA
 439 GAGGAGAGGT 1140
 E--> 441 ATATCTTCCA ACACCCACGG CCAAAGAAAC CAAAGTCGCT GAGAATATAT

3003

Done

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/056,454

DATE: 02/15/2002

TIME: 14:39:24

Input Set : A:\EP.txt

Output Set : N:\CRF3\02152002\J056454.raw

442 GAATCTCATA 1200

E--> 444 TTGGAATGAG TAGTCCGGAG CCTAAAATTA ACTCATACGT GAATTTTAGA
445 GATGAAGTTC 1260

E--> 447 TTCCTCGCAT AAAAAAGCTT GGGTACAATG CGCTGCGAAT TATGGCTATT
448 CAAGAGCATT 1320

E--> 450 CTTATTATGC TAGTTTTGGT TATCATGTCA CAAATTTTTT TGCACCAAGC
451 AGCCGTTTTG 1380

E--> 453 GAACGCCCGA CGACCTTAAG TCTTCGATTG ATAAAGCTCA TGAGCTAGGA
454 ATTGTTGTTC 1440

E--> 456 TCATGGACAT CGTTCACAGC CATGCATCAA ATAATACTTT AGATGGACTG
457 AACATGTTTG 1500

E--> 459 ACGGCACCGA TAGTTGTTAC TTTCACCTCG GAGCTCGTGG TTATCATTTG
460 ATGTGGGATT 1560

E--> 462 CCGCCTCTTT AACTATGGAA ACTGGGAGGT ACTTAGGTAT CTTCTCTCAA
463 ATGCGAGATG 1620

E--> 465 GTGGTTGGAT GAGTTCAAAT TTGATGGATT TAGATTCGAT GGTGTGACAT
466 CAATGATGTA 1680

E--> 468 TACTCACCAC GGATTATCGG TGGGATTAC TGGGAAC TAC GAGGAATACT
469 TTGGACTCGC 1740

E--> 471 AACTGATGTG GATGCTGTTG TGTATCTGAT GCTGGTCAAC GATCTTATTC
472 ATAGGCTTTT 1800

E--> 474 CCCAGATGCA ATTACCATTG GTGAAGATGT TAGCGGAATG CCGACATTTT
475 GTATTCCCGT 1860

E--> 477 TCAAGATGGG GGTGTTGGCT TTGACTATCG GCTGCATATG
478 GCAATTGCTG ATAAATGGAT 1920

E--> 480 TGAGTTGCTC AAGAAACGGG ATGAGGATTG GAGAGTGGGT
481 GATATTGTTC ATACACTGAC 1980

E--> 483 AAATAGAAGA TGGTCGGAAA AGTGTGTTTC ATACGCTGAA AGTCATGATC
484 AAGCTCTAGT 2040

E--> 486 CGGTGATAAA ACTATAGCAT TCTGGCTGAT GGACAAGGAT ATGTATGATT
487 TTATGGCTCT 2100

E--> 489 GGATAGACCG CCAACATCAT TAATAGATCG TGGGATAGCA TTGCACAAGA
490 TGATTAGGCT 2160

E--> 492 TGTAAC TATG GGATTAGGAG GAGAAGGGTA CCTAAATTTC ATGGGAAATG
493 AATTCGGCCA 2220

E--> 495 CCCTGAGTGG ATTGATTTC CTAGGGCTGA GCCACACCTT TCTGATGGCT
496 CAGTAATTC 2280

E--> 498 CGGAAACCAA TTCAGTTATG ATAAATGCAG ACGGAGATT
499 GACCTGGGAG ATGCAGAATA 2340

E--> 501 TTTAAGATAC CATGGGTTAC AAGAATTGTA CTGGGCTATG CAGTATCTTG
502 AAGATAAATA 2400

E--> 504 TGAGTTTATG ACTTCAGAAC ACCAGTTCAT ATCACGAAAG GATGAAGGAG
505 ATAGGATGAT 2460

E--> 507 TGTATTTGAA AGAGGAAACC TAGTTTTCGT CTTTAATTTT CACTGGACAA
508 ATAGCTATTC 2520

E--> 510 AGACTATCGC ATAGGCTGCC TGAAGCCTGG AAAATACAAG
511 GTTGTCTTGG ACTCAGATGA 2580

E--> 513 TCCACTTTTT GGTGGCTTCG GGAGAATTGA TCATAATGCC GAATATTTCA
514 CCTCTGAAGG 2640

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/056,454

DATE: 02/15/2002
TIME: 14:39:24

Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

E--> 516 ATCGTATGAT GATCGTCCTT GTTCAATTAT GGTGTATGCA CCTAGTAGAA
517 CAGCAGTGGT 2700

E--> 519 CTATGCACTA GTAGACAAAC TAGAAGTAGC AGTAGTAGAA GAACCCATTG
520 AAGAATGAAC 2760

E--> 522 GAACTTGTA TCGCGTTGAA AGATTGAAC GTTACTTGGT CATCCACATA
523 GAGCTTCTIG 2820

E--> 525 ACATCAGTCT TGGCGGAATT GCATGTGACA ACAAGGTTTG CAGTTCTTTT
526 CACTATTAGT 2880

E--> 528 AGTCCACCGA TATACGCAGA GATGAAGTGC TGAACAAACA TATGTAAAAA
529 CGATGAATTT 2940

E--> 531 ATGTCGAATG CTGGGACGAT CGAATTCCTG CAGCC

W--> 532 2975

534 (2) INFORMATION FOR SEQ ID NO: 14:
536 (i) SEQUENCE CHARACTERISTICS:
537 (A) LENGTH: 3033 base pairs
538 (B) TYPE: nucleic acid
539 (C) STRANDEDNESS: single
540 (D) TOPOLOGY: linear
544 (ix) FEATURE:
545 (A) NAME/KEY: CDS
546 (B) LOCATION:145..2790
549 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

E--> 551 TTGATGGGGC CTTGAACTCA GCAATTGAC ACTCAGTTAG TTACTACTCT
552 ATCACTTATC 60

E--> 554 AGATCTCTAT TTTTCTCTT AATTCCAACC AAGGAATGAA TAAAAGGATA
555 GATTGTGAAA 120

E--> 557 AACCCTAAGG AGAGAAGAAG AAAG ATG GTG TAT ACA CTC TCT GGA
558 GTT CGT 171

559 Met Val Tyr Thr Leu Ser Gly Val Arg
560 1 5

E--> 562 TTT CCT ACT GTT CCA TCA GTG TAC AAA TCT AAT GGA TTC AGC AGT
563 AAT 219

564 Phe Pro Thr Val Pro Ser Val Tyr Lys Ser Asn Gly Phe Ser Ser Asn
565 10 15 20 25

E--> 567 GGT GAT CGG AGG AAT GCT AAT GTT TCT GTA TTC TTG AAA AAG CAC
568 TCT 267

569 Gly Asp Arg Arg Asn Ala Asn Val Ser Val Phe Leu Lys Lys His Ser
570 30 35 40

E--> 572 CTT TCA CGG AAG ATC TTG GCT GAA AAG TCT TCT TAC AAT TCC GAA
573 TTC 315

574 Leu Ser Arg Lys Ile Leu Ala Glu Lys Ser Ser Tyr Asn Ser Glu Phe
575 45 50 55

E--> 577 CGA CCT TCT ACA GTT GCA GCA TCG GGG AAA GTC CTT GTG CCT GGA
578 ACC 363

579 Arg Pro Ser Thr Val Ala Ala Ser Gly Lys Val Leu Val Pro Gly Thr
580 60 65 70

E--> 582 CAG AGT GAT AGC TCC TCA TCC TCA ACA GAC CAA TTT GAG TTC ACT
583 GAG 411

584 Gln Ser Asp Ser Ser Ser Ser Ser Thr Asp Gln Phe Glu Phe Thr Glu

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Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

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      585      75      80      85
E--> 587 ACA TCT CCA GAA AAT TCC CCA GCA TCA ACT GAT GTA GAT AGT TCA
      588 ACA      459
      589 Thr Ser Pro Glu Asn Ser Pro Ala Ser Thr Asp Val Asp Ser Ser Thr
      590 90      95      100      105
E--> 592 ATG GAA CAC GCT AGC CAG ATT AAA ACT GAG AAC GAT GAC GTT GAG
      593 CCG      507
      594 Met Glu His Ala Ser Gln Ile Lys Thr Glu Asn Asp Asp Val Glu Pro
      595      110      115      120
E--> 597 TCA AGT GAT CTT ACA GGA AGT GTT GAA GAG CTG GAT TTT GCT TCA
      598 TCA      555
      599 Ser Ser Asp Leu Thr Gly Ser Val Glu Glu Leu Asp Phe Ala Ser Ser
      600      125      130      135
E--> 602 CTA CAA CTA CAA GAA GGT GGT AAA CTG GAG GAG TCT AAA ACA TTA
      603 AAT      603
      604 Leu Gln Leu Gln Glu Gly Gly Lys Leu Glu Glu Ser Lys Thr Leu Asn
      605      140      145      150
E--> 607 ACT TCT GAA GAG ACA ATT ATT GAT GAA TCT GAT AGG ATC AGA GAG
      608 AGG      651
      609 Thr Ser Glu Glu Thr Ile Ile Asp Glu Ser Asp Arg Ile Arg Glu Arg
      610      155      160      165
E--> 612 GGC ATC CCT CCA CCT GGA CTT GGT CAG AAG ATT TAT GAA ATA GAC
      613 CCC      699
      614 Gly Ile Pro Pro Pro Gly Leu Gly Gln Lys Ile Tyr Glu Ile Asp Pro
      615 170      175      180      185
E--> 617 CTT TTG ACA AAC TAT CGT CAA CAC CTT GAT TAC AGG TAT TCA CAG
      618 TAC      747
      619 Leu Leu Thr Asn Tyr Arg Gln His Leu Asp Tyr Arg Tyr Ser Gln Tyr
      620      190      195      200
E--> 622 AAG AAA CTG AGG GAG GCA ATT GAC AAG TAT GAG GGT GGT TTG GAA
      623 GCC      795
      624 Lys Lys Leu Arg Glu Ala Ile Asp Lys Tyr Glu Gly Gly Leu Glu Ala
      625      205      210      215
E--> 627 TTT TCT CGT GGT TAT GAA AAA ATG GGT TTC ACT CGT AGT GCT ACA
      628 GGT      843
      629 Phe Ser Arg Gly Tyr Glu Lys Met Gly Phe Thr Arg Ser Ala Thr Gly
      630      220      225      230
E--> 632 ATC ACT TAC CGT GAG TGG GCT CTT GGT GCC CAG TCA GCT GCC CTC
      633 ATT      891
      634 Ile Thr Tyr Arg Glu Trp Ala Leu Gly Ala Gln Ser Ala Ala Leu Ile
      635      235      240      245
E--> 637 GGA GAT TTC AAC AAT TGG GAC GCA AAT GCT GAC ATT ATG ACT CGG
      638 AAT      939
      639 Gly Asp Phe Asn Asn Trp Asp Ala Asn Ala Asp Ile Met Thr Arg Asn
      640 250      255      260      265
E--> 642 GAA TTT GGT GTC TGG GAG ATT TTT CTG CCA AAT AAT GTG GAT GGT
      643 TCT      987
      644 Glu Phe Gly Val Trp Glu Ile Phe Leu Pro Asn Asn Val Asp Gly Ser
      645      270      275      280

```

same

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/056,454

DATE: 02/15/2002

TIME: 14:39:24

Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

```

E--> 647 CCT GCA ATT CCT CAT GGG TCC AGA GTG AAG ATA CGT ATG GAC ACT
648 CCA 1035
649 Pro Ala Ile Pro His Gly Ser Arg Val Lys Ile Arg Met Asp Thr Pro
650 285 290 295
E--> 652 TCA GGT GTT AAG GAT TCC ATT CCT GCT TGG ATC AAC TAC TCT TTA
653 CAG 1083
654 Ser Gly Val Lys Asp Ser Ile Pro Ala Trp Ile Asn Tyr Ser Leu Gln
655 300 305 310
E--> 657 CTT CCT GAT GAA ATT CCA TAT AAT GGA ATA CAT TAT GAT CCA CCC
658 GAA 1131
659 Leu Pro Asp Glu Ile Pro Tyr Asn Gly Ile His Tyr Asp Pro Pro Glu
660 315 320 325
E--> 662 GAG GAG AGG TAT ATC TTC CAA CAC CCA CGG CCA AAG AAA CCA AAG
663 TCG 1179
664 Glu Glu Arg Tyr Ile Phe Gln His Pro Arg Pro Lys Lys Pro Lys Ser
665 330 335 340 345
E--> 667 CTG AGA ATA TAT GAA TCT CAT ATT GGA ATG AGT AGT CCG GAG CCT
668 AAA 1227
669 Leu Arg Ile Tyr Glu Ser His Ile Gly Met Ser Ser Pro Glu Pro Lys
670 350 355 360
E--> 672 ATT AAC TCA TAC GTG AAT TTT AGA GAT GAA GTT CTT CCT CGC ATA
673 AAA 1275
674 Ile Asn Ser Tyr Val Asn Phe Arg Asp Glu Val Leu Pro Arg Ile Lys
675 365 370 375
E--> 677 AAG CTT GGG TAC AAT GCG CTG CAA ATT ATG GCT ATT CAA GAG CAT
678 TCT 1323
679 Lys Leu Gly Tyr Asn Ala Leu Gln Ile Met Ala Ile Gln Glu His Ser
680 380 385 390
E--> 682 TAT TAC GCT AGT TTT GGT TAT CAT GTC ACA AAT TTT TTT GCA CCA
683 AGC 1371
684 Tyr Tyr Ala Ser Phe Gly Tyr His Val Thr Asn Phe Phe Ala Pro Ser
685 395 400 405
E--> 687 AGC CGT TTT GGA ACG CCC GAC GAC CTT AAG TCT TTG ATT GAT AAA
688 GCT 1419
689 Ser Arg Phe Gly Thr Pro Asp Asp Leu Lys Ser Leu Ile Asp Lys Ala
690 410 415 420 425
E--> 692 CAT GAG CTA GGA ATT GTT GTT CTC ATG GAC ATT GTT CAC AGC CAT
693 GCA 1467
694 His Glu Leu Gly Ile Val Val Leu Met Asp Ile Val His Ser His Ala
695 430 435 440
E--> 697 TCA AAT AAT ACT TTA GAT GGA CTG AAC ATG TTT GAC TGC ACC GAT
698 AGT 1515
699 Ser Asn Asn Thr Leu Asp Gly Leu Asn Met Phe Asp Cys Thr Asp Ser
700 445 450 455
E--> 702 TGT TAC TTT CAC TCT GGA GCT CGT GGT TAT CAT TGG ATG TGG GAT
703 TCC 1563
704 Cys Tyr Phe His Ser Gly Ala Arg Gly Tyr His Trp Met Trp Asp Ser
705 460 465 470
E--> 707 CGC CTC TTT AAC TAT GGA AAC TGG GAG GTA CTT AGG TAT CTT CTC

```

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```

708 TCA      1611
709 Arg Leu Phe Asn Tyr Gly Asn Trp Glu Val Leu Arg Tyr Leu Leu Ser
710      475      480      485
E--> 712 AAT GCG AGA TGG TGG TTG GAT GCG TTC AAA TTT GAT GGA TTT AGA
713 TTT      1659
714 Asn Ala Arg Trp Trp Leu Asp Ala Phe Lys Phe Asp Gly Phe Arg Phe
715 490      495      500      505
E--> 717 GAT GGT GTG ACA TCA ATG ATG TAT ATT CAC CAC GGA TTA TCG GTG
718 GGA      1707
719 Asp Gly Val Thr Ser Met Met Tyr Ile His His Gly Leu Ser Val Gly
720      510      515      520
E--> 722 TTC ACT GGG AAC TAC GAG GAA TAC TTT GGA CTC GCA ACT GAT GTG
723 GAT      1755
724 Phe Thr Gly Asn Tyr Glu Glu Tyr Phe Gly Leu Ala Thr Asp Val Asp
725      525      530      535
E--> 727 GCT GTT GTG TAT CTG ATG CTG GTC AAC GAT CTT ATT CAT GGG CTT
728 TTC      1803
729 Ala Val Val Tyr Leu Met Leu Val Asn Asp Leu Ile His Gly Leu Phe
730      540      545      550
E--> 732 CCA GAT GCA ATT ACC ATT GGT GAA GAT GTT AGC GGA ATG CCG ACA
733 TTT      1851
734 Pro Asp Ala Ile Thr Ile Gly Glu Asp Val Ser Gly Met Pro Thr Phe
735      555      560      565
E--> 737 TGT ATT CCC GTC CAA GAG GGG GGT GTT GGC TTT GAC TAT CGG CTG
738 CAT      1899
739 Cys Ile Pro Val Gln Glu Gly Gly Val Gly Phe Asp Tyr Arg Leu His
740 570      575      580      585
E--> 742 ATG GCA ATT GCT GAT AAA CGG ATT GAG TTG CTC AAG AAA CGG GAT
743 GAG      1947
744 Met Ala Ile Ala Asp Lys Arg Ile Glu Leu Leu Lys Lys Arg Asp Glu
745      590      595      600
E--> 747 GAT TGG AGA GTG GGT GAT ATT GTT CAT ACA CTG ACA AAT AGA AGA
748 TGG      1995
749 Asp Trp Arg Val Gly Asp Ile Val His Thr Leu Thr Asn Arg Arg Trp
750      605      610      615
E--> 752 TCG GAA AAG TGT GTT TCA TAC GCT GAA AGT CAT GAT CAA GCT CTA
753 GTC      2043
754 Ser Glu Lys Cys Val Ser Tyr Ala Glu Ser His Asp Gln Ala Leu Val
755      620      625      630
E--> 757 GGT GAT AAA ACT ATA GCA TTC TGG CTG ATG GAC AAG GAT ATG TAT
758 GAT      2091
759 Gly Asp Lys Thr Ile Ala Phe Trp Leu Met Asp Lys Asp Met Tyr Asp
760      635      640      645
E--> 762 TTT ATG GCT CTG GAT AGA CCG TCA ACA TCA TTA ATA GAT CGT GGG
763 ATA      2139
764 Phe Met Ala Leu Asp Arg Pro Ser Thr Ser Leu Ile Asp Arg Gly Ile
765 650      655      660      665
E--> 767 GCA TTG CAC AAG ATG ATT AGG CTT GTA ACT ATG GGA TTA GGA GGA
768 GAA      2187

```

Done

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```

769 Ala Leu His Lys Met Ile Arg Leu Val Thr Met Gly Leu Gly Gly Glu
770                               670           675           680
E--> 772 GGG TAC CTA AAT TTC ATG GGA AAT GAA TTC GGC CAC CCT GAG TGG
773 ATT                2235
774 Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Ile
775                               685           690           695
E--> 777 GAT TTC CCT AGG GCT GAA CAA CAC CTC TCT GAT GGC TCA GTA ATC
778 CCC                2283
779 Asp Phe Pro Arg Ala Glu Gln His Leu Ser Asp Gly Ser Val Ile Pro
780                               700           705           710
E--> 782 GGA AAC CAA TTC AGT TAT GAT AAA TGC AGA CGG AGA TTT GAC CTG
783 GGA                2331
784 Gly Asn Gln Phe Ser Tyr Asp Lys Cys Arg Arg Arg Phe Asp Leu Gly
785                               715           720           725
E--> 787 GAT GCA GAA TAT TTA AGA TAC CGT GGG TTG CAA GAA TTT GAC CGG
788 CCT                2379
789 Asp Ala Glu Tyr Leu Arg Tyr Arg Gly Leu Gln Glu Phe Asp Arg Pro
790                               730           735           740           745
E--> 792 ATG CAG TAT CTT GAA GAT AAA TAT GAG TTT ATG ACT TCA GAA CAC
793 CAG                2427
794 Met Gln Tyr Leu Glu Asp Lys Tyr Glu Phe Met Thr Ser Glu His Gln
795                               750           755           760
E--> 797 TTC ATA TCA CGA AAG GAT GAA GGA GAT AGG ATG ATT GTA TTT GAA
798 AAA                2475
799 Phe Ile Ser Arg Lys Asp Glu Gly Asp Arg Met Ile Val Phe Glu Lys
800                               765           770           775
E--> 802 GGA AAC CTA GTT TTT GTC TTT AAT TTT CAC TGG ACA AAA AGC TAT
803 TCA                2523
804 Gly Asn Leu Val Phe Val Phe Asn Phe His Trp Thr Lys Ser Tyr Ser
805                               780           785           790
E--> 807 GAC TAT CGC ATA GCC TGC CTG AAG CCT GGA AAA TAC AAG GTT GCC
808 TTG                2571
809 Asp Tyr Arg Ile Ala Cys Leu Lys Pro Gly Lys Tyr Lys Val Ala Leu
810                               795           800           805
E--> 812 GAC TCA GAT GAT CCA CTT TTT GGT GGC TTC GGG AGA ATT GAT CAT
813 AAT                2619
814 Asp Ser Asp Asp Pro Leu Phe Gly Gly Phe Gly Arg Ile Asp His Asn
815                               815           820           825
E--> 817 GCC GAA TAT TTC ACC TTT GAA GGA TGG TAT GAT GAT CGT CCT CGT
818 TCA                2667
819 Ala Glu Tyr Phe Thr Phe Glu Gly Trp Tyr Asp Asp Arg Pro Arg Ser
820                               830           835           840
E--> 822 ATT ATG GTG TAT GCA CCT TGT AAA ACA GCA GTG GTC TAT GCA CTA
823 GTA                2715
824 Ile Met Val Tyr Ala Pro Cys Lys Thr Ala Val Val Tyr Ala Leu Val
825                               845           850           855
E--> 827 GAC AAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GTA GCA
828 GCA                2763
829 Asp Lys Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Val Ala Ala

```

Done

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```

      830          860          865          870
E--> 832 GTA GAA GAA GTA GTA GTA GAA GAA GAA TGAACGAACT TGTGATCGCG
W--> 833 2810
      834 Val Glu Glu Val Val Val Glu Glu Glu
W--> 835      875          880
E--> 837 TTGAAAGATT TGAACGCTAC ATAGAGCTTC TTGACGTATC TGGCAATATT
      838 GCATCAGTCT      2870
E--> 840 TGGCGGAATT TCATGTGACA CAAGGTTTGC AATTCTTTCC ACTATTAGTA
      841 GTGCAACGAT      2930
E--> 843 ATACGCAGAG ATGAAGTGCT GAACAAACAT ATGTAAAATC GATGAATTTA
      844 TGTCGAATGC      2990
E--> 846 TGGGACGATC GAATTCCTGC AGGCCGGGGG ACCCCTTAGT TCT
W--> 847 3033
      1028 (2) INFORMATION FOR SEQ ID NO: 16:
      1030 (i) SEQUENCE CHARACTERISTICS:
      1031 (A) LENGTH: 2576 base pairs
      1032 (B) TYPE: nucleic acid
      1033 (C) STRANDEDNESS: single
      1034 (D) TOPOLOGY: linear
      1040 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
E--> 1042 TCATTAAAGA GGAGAAATTA ACTATGAGAG GATCTCACCA TCACCATCAC
      1043 CATGGGATCT      60
E--> 1045 TGGCTGAAAA GTCTTCTTAC AATTCCGAAT TCCGACCTTC TACAGTTGCA
      1046 GCATCGGGGA      120
E--> 1048 AAGTCCTTGT GCCTGGAACC CAGAGTGATA GCTCCTCATC CTCAACAAAC
      1049 CAATTTGAGT      180
E--> 1051 TCACCTGAGAC ATCTCCAGAA AATCCCCCAG CATCAACTGA TGTAGATAGT
      1052 TCAACAATGG      240
E--> 1054 AACACGCTAG CCAGATTAAA ACTGAGAACG ATGACGTTGA
      1055 GCCGTCAAGT GATCTTACAG      300
E--> 1057 GAAGTGTTGA AGAGCTGGAT TTTGCTTCAT CACTACAACT ACAAGAAGGT
      1058 GGTAACTGG      360
E--> 1060 AGGAGTCTAA AACATTAAAT ACTTCTGAAG AGACAATTAT TGATGAATCT
      1061 GATAGGATCA      420
E--> 1063 GAGAGAGGGG CATCCCTCCA CCTGGACTTG GTCAGAAGAT
      1064 TTATGAAATA GACCCCTTT      480
E--> 1066 TGACAAACTA TCGTCAACAC CTTGATTACA GGTATTACAC GTACAAGAAA
      1067 CTGAGGGGAGG      540
E--> 1069 CAATTGACAA GTATGAGGGT GGTGTGAAG CTTTCTCTCG TGGTTATGAA
      1070 AAAATGGGTT      600
E--> 1072 TCACCTCGTAG TGCTACAGGT ATCACTTACC GTGAGTGGGC
      1073 TCCTGGTGCC CAGTCAGCTG      660
E--> 1075 CCCTCATTGG AGATTTCAAC AATTGGGACG CAAATGCTGA CATTATGACT
      1076 CGGAATGAAT      720
E--> 1078 TTGGTGCTCTG GGAGATTTTT CTGCCAAATA ATGTGGATGG TTCTCCTGCA
      1079 ATTCCTCATG      780
E--> 1081 GGTCCAGAGT GAAGATACGT ATGGACACTC CATCAGGTGT
      1082 TAAGGATTCC ATTCCTGCTT      840
E--> 1084 GGATCAACTA CTCTACAGCT TCCTGATGAA ATTCCATATA ATGGAATATA

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Done

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```

1085 TTATGATCCA      900
E--> 1087 CCCGAAGAGG AGAGGTATAT CTTCCAACAC CCACGGCCAA
1088 AGAAACCAAA GTCGCTGAGA      960
E--> 1090 ATATATGAAT CTCATATTGG AATGAGTAGT CCGGAGCCTA AAATTAACCTC
1091 ATACGTGAAT      1020
E--> 1093 TTTAGAGATG AAGTTCTTCC TCGCATAAAA AAGCTTGGGT ACAATGCGCT
1094 GCAAAATTATG      1080
E--> 1096 GCTATTCAAG AGCATTCTTA TTATGCTAGT TTTGGTTATC ATGTCACAAA
1097 TTTTTTTGCA      1140
E--> 1099 CCAAGCAGCC GTTTTGGAAAC GCCCCGACGAC CTTAAGTCTT TGATTGATAA
1100 AGCTCATGAG      1200
E--> 1102 CTAGGAATTG TTGTTCTCAT GGACATTGTT CACAGCCATG CATCAAATAA
1103 TACTTTAGAT      1260
E--> 1105 GGACTGAACA TGTTTGACGG CACCGATAGT TGTTACTTTC ACTCTGGAGC
1106 TCGTGGTTAT      1320
E--> 1108 CATTGGATGT GGGATTCCCG CCTTTTAAAC TATGGAACT GGGAGGTACT
1109 TAGGTATCTT      1380
E--> 1111 CTCTCAAATG CGAGATGGTG GTTGGATGAG TTCAAATTG ATGGATTTAG
1112 ATTTGATGGT      1440
E--> 1114 GTGACATCAA TGATGTATAC TCACCACGGA TTATCGGTGG GATTCACTGG
1115 GAACTACGAG      1500
E--> 1117 GAATACTTTG GACTCGCAAC TGATGTGGAT GCTGTTGTGT ATCTGATGCT
1118 GGTCAACGAT      1560
E--> 1120 CTTATTTCAT GGGTTTTCCC AGATGCAATT ACCATTGGTG AAGATGTTAG
1121 CGGAATGCCG      1620
E--> 1123 ACATTTTGTA TTCCCGTTCA AGATGGGGGT GTTGGCTTTG ACTATCGGCT
1124 GCATATGGCA      1680
E--> 1126 ATTGCTGATA AATGGATTGA GTTGCTCAAG AAACGGGATG
1127 AGGATTGGAG AGTGGGTGAT      1740
E--> 1129 ATTGTTTATA CACTGACAAA TAGAAGATGG TCGGAAAAGT GTGTTTCATA
1130 CGCTGAAAAGT      1800
E--> 1132 CATGATCAAG CTCTAGTCGG TGATAAACT ATAGCATCTCT GGCTGATGGA
1133 CAAGGATATG      1860
E--> 1135 TATGATTTTA TGGCTCTGGA TAGACCGCCA ACATCATTA TAGATCGTGG
1136 GATAGCATTG      1920
E--> 1138 CACAAGATGA TTAGGCTTGT AACTATGGGA TTAGGAGGAG
1139 AAGGGTACCT AAATTTTCATG      1980
E--> 1141 GGAAATGAAT TCGGCCACCC TGAGTGGATT GATTTCCTTA
1142 GGGCTGAACA ACACCTCTCT      2040
E--> 1144 GATGACTCAG TAATTTCCCG AAACCAATTC AGTTATGATA AATGCAGACG
1145 GAGATTGAC      2100
E--> 1147 CTGGGAGATG CAGAATATTT AAGATACCGT GGGTTGCAAG AATTTGACCG
1148 GGCTATGCGAG      2160
E--> 1150 TATCTTGAAG ATAAATATGA GTTTATGACT TCAGAACACC AGTTTCATATC
1151 ACGAAAGGAT      2220
E--> 1153 GAAGGAGATA GGATGATTGT ATTTGAAAAA GGAAACCTAG TTTTGTCTT
1154 TAATTTTCAC      2280
E--> 1156 TGGACAAAAA GCTATTCAGA CTATCGCATA GGCTGCCTGA AGCCTGGAAA
1157 ATACAAGGTT      2340

```

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```

E--> 1159 GCCTTGGACT CAGATGATCC ACTTTTGGT GGCTTCGGGA GAATTGATCA
      1160 TAATGCCGAA      2400
E--> 1162 TATTTACCTT TTGAAGGATG GTATGATGAT CGTCCTCGTT CAATTATGGT
      1163 GTATGCACCT      2460
E--> 1165 TGTAGAACAG CAGTGGTCTA TGCACTAGTA GACAAAGAAG
      1166 AAGAAGAAGA AGAAGAAGAA      2520
E--> 1168 GAAGAAGTAG CAGTAGTAGA AGAAGTAGTA GTAGAAGAAG
      1169 AATGAACGAA CTTGTG      2576
      1171 (2) INFORMATION FOR SEQ ID NO: 17:
      1173 (i) SEQUENCE CHARACTERISTICS:
      1174 (A) LENGTH: 2529 base pairs
      1175 (B) TYPE: nucleic acid
      1176 (C) STRANDEDNESS: single
      1177 (D) TOPOLOGY: linear
      1183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
E--> 1185 GGATGCTAAT GTTCTGTAT TCTTGAAAA GCACCTCTCTT TCACGGAAGA
      1186 TCTTGGCTGA      60
E--> 1188 AAAGTCTTCT TACAATTCCG AATCCCGACC TTCTACAGTT GCAGCATCGG
      1189 GGAAAGTCCT      120
E--> 1191 TGTGCCTGGA AYCCAGAGTG ATAGCTCCTC ATCCTCAACA GACCAATTGT
      1192 AGTTCCTGTA      180
E--> 1194 GACATCTCCA GAAAAATTCCC CAGCATCAAC TGATGTAGAT AGTTCAACAA
      1195 TGGACACGC      240
E--> 1197 TAGCCAGATT AAAACTGAGA ACGATGACGT TGAGCCGTCA AGTGATCTTA
      1198 CAGGAAGTGT      300
E--> 1200 TGAAGAGCTG GATTTTGCTT CATCACTACA ACTACAAGAA GGTGGTAAAC
      1201 TGGAGGAGTC      360
E--> 1203 TAAACATTA AATACTTCTG AAGAGACAAT TATTGATGAA TCTGATAGGA
      1204 TCAGAGAGAG      420
E--> 1206 GGGCATCCCT CCACCTGGAC TTGGTCAGAA GATTTATGAA
      1207 ATAGACCCCC TTTTGACAAA      480
E--> 1209 CTATCGTCAA CACCTTGATT ACAGGTATTC ACAGTACAAG AAAGTGAGGG
      1210 AGGCAATTGA      540
E--> 1212 CAAGTATGAG GGTGGTTTGG AAGCTTTTTC TCGTGTTTAT GAAAAATG
      1213 GTTTCCTCG      600
E--> 1215 TAGTGCTACA GGTATCACTT ACCGTGAGTG GGCTCCTGGT
      1216 GCCCAGTCAG CTGCCCTCAT      660
E--> 1218 TGGAGATTTC AACAATTGGG ACGCAAATGC TGACATTATG ACTCGGAATG
      1219 AATTGGTGT      720
E--> 1221 CTGGGAGATT TTTCTGCCAA ATAATGTGGA TGGTTCTCCT GCAATTCCTC
      1222 ATGGGTCCAG      780
E--> 1224 AGTGAAGATA CGYATGGACA CTCCATCAGG TGTTAAGGAT TCCATTCCTG
      1225 CTGGATCAA      840
E--> 1227 CTACTCTTTA CAGCTTCCTG ATGAAATTCC ATATAATGGA ATATATTATG
      1228 ATCCACCCGA      900
E--> 1230 AGAGGAGAGG TATRTCTTCC AACACCCACG GCCAAAGAAA
      1231 CCAAAGTCGC TGGAATATA      960
E--> 1233 TGAATCTCAT ATTGGAATGA GTAGTCCGGA GCCTAAAATT AACTCATACG
      1234 TGAATTTAG      1020

```

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Input Set : A:\EP.txt

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E--> 1236 AGATGAAGTT CTCCTCGCA TAAAAASCT TGGGTACAAT GCGGTGCAAA
 1237 TTATGGCTAT 1080
 E--> 1239 TCAAGAGCAT TCTTATTATG CTAGTTTGG TTATCATGTC ACAAATTTT
 1240 TTGCACCAAG 1140
 E--> 1242 CAGCCGTTTT GGAACGCCG ACGACCTTAA GTCTTTGATT GATAAAGCTC
 1243 ATGAGCTAGG 1200
 E--> 1245 AATTGTGTGT CTCATGGACA TTGTTACAG CCATGCATCA AATAATACTT
 1246 TAGATGGACT 1260
 E--> 1248 GAACATGTTT GACGGCACAG ATAGTTGTTA CTTTCACTCT GGAGCTCGTG
 1249 GTTATCATTG 1320
 E--> 1251 GATGTGGGAT TCCCGCTCT TTAACATAG AACTGGGAG GTACTTAGGT
 1252 ATCTTCTCTC 1380
 E--> 1254 AAATGCGAGA TGGTGGTTGG ATGAGTTCAA ATTTGATGGA TTTAGATTG
 1255 ATGGTGTGAC 1440
 E--> 1257 ATCAATGATG TATACTCACC ACGGATTATC GGTGGGATTC ACTGGGAAC
 1258 ACGAGGAATA 1500
 E--> 1260 CTTTGGACTC GCAACTGATG TGGATGCTGT TGTGTATCTG ATGCTGGTCA
 1261 ACGATCTTAT 1560
 E--> 1263 TCACGGGCTT TTCCAGATG CAATTACCAT TGGTGAAGAT GTTAGCGGAA
 1264 TGCCGACATT 1620
 E--> 1266 TTGTATTCCC GTTCAAGATG GGGGTGTTGG CTTTGAATAT CGGCTGCATA
 1267 TGGCAATTGC 1680
 E--> 1269 TGATAAATGG ATGAGTTGC TCAAGAAACG GGATGAGGAT
 1270 TGGAGAGTGG GTGATATTGT 1740
 E--> 1272 TCATACACTG ACAAATAGAA GATGGTCGGA AAAGTGTGTT TCATMCGCTG
 1273 AAAGTCATGA 1800
 E--> 1275 TCAAGCTCTA GTCGGTGATA AACTATAGC ATYCTGGCTG ATGACAAGG
 1276 ATATGTATGA 1860
 E--> 1278 TTTTATGGCT CTGGATAGAC CGYCAACAYC ATTAATAGAT CGTGGGATAG
 1279 CATTGCACAA 1920
 E--> 1281 GATGATTAGG CTGTAACTA TGGGATTAGG AGGAGAAGGG TACCTAAATT
 1282 TCATGGGAAA 1980
 E--> 1284 TGAATTCGGC CACCCTGAGT GGATTGATTT CCCTAGGGCT
 1285 GARCAACACC TCTCTGATGG 2040
 E--> 1287 CTCAGTAATT CCCGAAACC AATTCAGTTA TGATAAATGC AGACGGAGAT
 1288 TTGACCTGGG 2100
 E--> 1290 AGATGCAGAA TATTTAAGAT ACCATGGGTT GCAAGAATTT GACCGGGCTA
 1291 TGCAGTATCT 2160
 E--> 1293 TGAAGATAAA TATGAGTTTA TGAATTCAGA ACACCAAGTT ATATCACGAA
 1294 AGGATGAAGG 2220
 E--> 1296 AGATAGGATG ATGTATTG AAARAGGAAA CCTAGTTTTT GTCTTTAATT
 1297 TTCCTGGAC 2280
 E--> 1299 AAATAGCTAT TCAGACTATC GCATAGGCTG CCTGAAGCCT GGAATAACA
 1300 AGGTGGCTT 2340
 E--> 1302 GGAATCAGAT GATCCACTTT TTGGTGGCTT CGGGAGAATT GATCATAATG
 1303 CCGAATATTT 2400
 E--> 1305 CACCTCTGAA GGATCGTATG ATGATCGTCC TCGTTCAATT ATGGTGTATG
 1306 CACCTAGTAG 2460
 E--> 1308 AACAGCAGTG GTCTATGCAC TAGTAGACAA ANTAGAAGNA

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```

1309 GAAGAAGAAG AAGAANCCGN      2520
1311 NGAAGAATT
1313 (2) INFORMATION FOR SEQ ID NO: 18:
1315     (i) SEQUENCE CHARACTERISTICS:
1316         (A) LENGTH: 3231 base pairs
1317         (B) TYPE: nucleic acid
1318         (C) STRANDEDNESS: single
1319         (D) TOPOLOGY: linear
1325     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
E--> 1327 GATTTAATAC GACTCACTAT AGGGATTTTT TTTT TTTT TTTTAAAAAC
1328 CTCCTCCACT      60
E--> 1330 CAGTCTTGGG ATCTCTCTCT CTCTTCACGC TTCTCTTGGG GCCTTGAAC
1331 CAGCAATTTG      120
E--> 1333 ACACCTCAGT AGTTACACTC CTATCACTCA TCAGATCTCT ATTTTCTCTC
1334 TTAATTCCAA      180
E--> 1336 CCAAGGAATG AATTAAGAAG TTAGATTGTA AGGAGAGAAG AAGAAAGATG
1337 GTGTATACAC      240
E--> 1339 TCTCTGGAGT TCGTTTTCCCT ACTGTTCCAT CAGTGATCAA ATCTAATGGA
1340 TTCAGCAGTA      300
E--> 1342 ATGGTGATCG GAGGAATGCT AATGTTTCTG TATTCTTGAA AAAGCACTCT
1343 CTTTCACGGA      360
E--> 1345 AGATCTTGGC TGAAGAAGTCT TCTTACGATT CCGAATCCCG ACCTTCTACA
1346 GTTGCAGCAT      420
E--> 1348 CGGGGAAAAGT CCTTGTTACCT GGAATCCAGA GTGATAGCTC
1349 CTCATCCTCA ACAGACCAAT      480
E--> 1351 TTGAGTTCAC TGAGACAGCT CCAGAAAATT CCCCAGCATC AACTGATGTG
1352 GATAGTTCAA      540
E--> 1354 CAATGGAACA CGCTAGCCAG ATTAAGAACTG AGAACGATGA
1355 CGTTGAGCCG TCAAGTGATC      600
E--> 1357 TTACAGGAAG TGTGAAGAG TTGGATTTTG CTTCACTACT ACAACTACAA
1358 GAAGGTGGTA      660
E--> 1360 AACTGGAGGA GTCTAAAACA TTAAATACTT CTGAAGAGAC AATTATTGAT
1361 GAATCTGATA      720
E--> 1363 GGATCAGAGA GAGGGGCAATC CCTCCACCTG GACTTGGTCA
1364 GAAGATTTAT GAAATAGACC      780
E--> 1366 CCCTTTTGAC AAACATCGT CAACACCTTG ATTACAGGTA TTCACAGTAC
1367 AAGAAAATGA      840
E--> 1369 GGGAGGCAAT TGACAAGTAT GAGGGTGGTT TGGGAAGCTTT
1370 TTCTCGTGGT TATGAAGAAA      900
E--> 1372 TGGGTTTCAC TCGTAGTGCT ACAGGTATCA CTTACCGTGA GTGGGCTCCT
1373 GGTGCCAGT      960
E--> 1375 CAGCTGCTCT CATTTGGAGT TTCAACAATT GGGACGCAAA TGCTGACATT
1376 ATGACTCGGA      1020
E--> 1378 ATGAATTTGG TGTCTGGGAG ATTTTCTGCG CAAATAATGT GGATGGTTCT
1379 CTGCAATTC      1080
E--> 1381 CTCATGGGTC CAGAGTGAAG ATACGCATGG ACACTTCATC
1382 AGGTGTTAAG GATTCCATTC      1140
E--> 1384 CTGCTTGGAT CAACTACTCT TTACAGCTTC CTGATGAAT TCCATATAAT
1385 GGAATATATT      1200

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2529

Done

RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/056,454

TIME: 14:39:24

Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

E--> 1387 ATGATCCACC CGAAGAGGAG AGGTATGTCT TCCAACACCC
 1388 ACGGCCAAAG AAACCAAAGT 1260
 E--> 1390 CGCTGAGAA ATATGAATCT CATATTGGAA TGAGTAGTCC GGAGCCTAAA
 1391 ATTAATCAT 1320
 E--> 1393 ACGTGAATTT TAGAGATGAA GTTCTTCCTC GCATAAAAAA CCTTGGGTAC
 1394 AATGCGGTGC 1380
 E--> 1396 AAATTATGGC TATTCGAAG CATCTTATT ATGCTAGTTT TGGTTATCAT
 1397 GTCACAAAT 1440
 E--> 1399 TTTTTCGACC AAGCAGCCGT TTTGGAACGC CCGACGACCT TAAGTCTTTG
 1400 ATTGATAAAG 1500
 E--> 1402 CTCATGAGCT AGGAATGTGT GTTCTCATGG ACATTGTTC AAGCCATGCA
 1403 TCAATAATA 1560
 E--> 1405 CTTTAGATGG ACTGAACATG TTTGACGGCA CAGATAGTTG TTACTTTCAC
 1406 TCTGGAGCTC 1620
 E--> 1408 GTGGTTATCA TTGGATGTGG GATTCCCGCC TCTTTAACTA TGGAAACTGG
 1409 GAGGTACTTA 1680
 E--> 1411 GGTATCTTCT CTCAATGCG AGATGGTGGT TGGATGAGTG CAAATTTGRT
 1412 GGATTAGAT 1740
 E--> 1414 TTGATGGTGT GACATCAATG ATGTATACTC ACCACGGATT ATCGGTGGGA
 1415 TTTACTGGGA 1800
 E--> 1417 ACTACGAGGA ATACTTTGGA CTCGCAACTG ATGTRGATGC TGCCGTGTAT
 1418 CTGATGCTGG 1860
 E--> 1420 CCAACGATCT TATTCATGGG CTTTCCAG ATGCAATTAC CATTGGTGAA
 1421 GATGTTAGCG 1920
 E--> 1423 GAATGCCGAC ATTTTGTATT CCCGTTCAAG ATGGGGGTGT TGGCTTTGAC
 1424 TATCGGCTGC 1980
 E--> 1426 ATATGGCAAT TGCTGATAAA TGGATTGAGT TGCTCAAGAA ACGGGATGAG
 1427 GATTGGAGAG 2040
 E--> 1429 TGGGTGATAT TGTTCAATCA CTGACAAATA GAAGATGGTC GGAAGAGTGT
 1430 GTTTCATACG 2100
 E--> 1432 CTGAAAGTCA TGATCAAGCT CTAGTCGGTG ATAAACTAT AGCATTCTGG
 1433 CTGATGGACA 2160
 E--> 1435 AGGATATGTA TGATTTTATG GCTTTGGATA GACCGTCAAC ATCATTATA
 1436 GATCGTGGGA 2220
 E--> 1438 TAGCATTGCA CAAGATGATT AGGCTTGTA CTATGGGATT AGGAGGAGAA
 1439 GGGTACCTAA 2280
 E--> 1441 ATTTTCATGGG AAATGAATTC GGCCACCCTG AGTGGATTGA TTTCCCTAGG
 1442 GCTGAACAAC 2340
 E--> 1444 ACCTCTCTGA TGGCTCAGTA ATTCCCGGAA ACCAATTGAG TTATGATAAA
 1445 TGCAGACGGA 2400
 E--> 1447 GATTTGACCT GGGAGATGCA GAATATTTAA GATACCGTGG GTTGCAAGAA
 1448 TTTGACCGGG 2460
 E--> 1450 CTATGCAGTA TCTTGAAGAT AAATATGAGT TTATGACTTC AGAACACCAG
 1451 TTCATATCAC 2520
 E--> 1453 GAAAGGATGA AGGAGATAGG ATGATTGTAT TTGAAAAAGG AAACCTAGTT
 1454 TTTGTCTTTA 2580
 E--> 1456 ATTTTCACTG GACAAAAAGC TATTCAGACT ATCGCATAGG CTGGCTGAAG
 1457 CCTGGAAAAT 2640
 E--> 1459 ACAAGGTTGC CTTGGACTCA GATGATCCAC TTTTGGTGG

none

RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/056,454

TIME: 14:39:24

Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

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1460 CTTCCGGGAGA ATTGATCATA      2700
E--> 1462 ATGCCGAATG TTTCACCTTT GAAGGATGGT ATGATGATCG TCCTCGTTCA
1463 ATTATGGTGT      2760
E--> 1465 ATGCACCTAG TAGAACAGCA GTGGTCTATG CACTAGTAGA CAAAGAAGAA
1466 GAAGAAGAAG      2820
E--> 1468 AAGTAGCAGT AGTAGAAGAA GTAGTAGTAG AAGAAGAATG AACGAACTTG
1469 TGATCGCGTT      2880
E--> 1471 GAAAGATTTC AACGCTACAT AGAGCTTCTT GACGTATCTG GCAATATTGC
1472 ATCAGTCTTG      2940
E--> 1474 GCGGAATTTT ATGTGACAAA AGGTTTGCAA TTCTTTCCAC TATTAGTAGT
1475 GCAACGATAT      3000
E--> 1477 ACGCAGAGAT GAAGTGCTGA ACAAACATAT GTAAAATCGA TGAATTTATG
1478 TCGAATGCTG      3060
E--> 1480 GGACGGGCTT CAGCAGGTTT TGCTTAGTGA GTTCTGTAAA TTGTCATCTC
1481 TTTANATGTA      3120
E--> 1483 CAGCCCACTA GAAATCAATT ATGTGAGACC TAAAAACAA TAACCATAAA
1484 ATGGAAATAG      3180
E--> 1486 TGCTGATCTA ATGATGTTTT AANCCNNNNA AAAAAAAAAA AAAAACTCGA
1487 G      3231
1489 (2) INFORMATION FOR SEQ ID NO: 19:
1491 (i) SEQUENCE CHARACTERISTICS:
1492 (A) LENGTH: 2578 base pairs
1493 (B) TYPE: nucleic acid
1494 (C) STRANDEDNESS: single
1495 (D) TOPOLOGY: linear
1501 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
E--> 1503 TCATTAAAGA GGAGAAATTA ACTATGAGAG GATCTCACCA TCACCATCAC
1504 CATGGGATCT      60
E--> 1506 TGGCTGAAAA GTCTTCTTAC AATTCCGAAT TCCGACCTTC TACAGTTGCA
1507 GCATCGGGGA      120
E--> 1509 AAGTCCTTGT GCCTGGAACC CAGAGTGATA GCTCCTCATC CTCAACAAAC
1510 CAATTGAGT      180
E--> 1512 TCACCTGAGAC ATCTCCAGAA AATTCCCCAG CATCAACTGA TGTAGATAGT
1513 TCAACAATGG      240
E--> 1515 AACACGCTAG CCAGATTAAA ACTGAGAACG ATGACGTTGA
1516 GCCGTCAAGT GATCTTACAG      300
E--> 1518 GAAGTGTTGA AGAGCTGGAT TTTGCTTCAT CACTACAACT ACAAGAAGGT
1519 GGTAAACTGG      360
E--> 1521 AGGAGTCTAA AACATTAAAT ACTTCTGAAG AGACAATTAT TGATGAATCT
1522 GATAGGATCA      420
E--> 1524 GAGAGAGGGG CATCCCTCCA CCTGGACTTG GTCAGAAGAT
1525 TTATGAAATA GACCCCTTT      480
E--> 1527 TGACAACTA TCGTCAACAC CTTGATTACA GGTATTACAC GTACAAGAAA
1528 CTGAGGGAGG      540
E--> 1530 CAATTGACAA GTATGAGGGT GGTTTGGAAG CTTTTTCTCG TGTTATGAA
1531 AAAATGGGTT      600
E--> 1533 TCACTCGTAG TGCTACAGGT ATCACTTACC GTGAGTGGGC
1534 TCCTGGTGCC CAGTCAGCTG      660
E--> 1536 CCCTCATTGG AGATTTCAAC AATTGGGACG CAAATGCTGA CATTATGACT

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*Done**Done*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/056,454

DATE: 02/15/2002
TIME: 14:39:24

Input Set : A:\EP.txt
Output Set: N:\CRF3\02152002\J056454.raw

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1537 CGGAATGAAT      720
E--> 1539 TTGGTGCTGTG GGAGATTTT CTGCCAATA ATGTGGATGG TTCTCCTGCA
1540 ATTCTCATG      780
E--> 1542 GGTCCAGAGT GAAGATACGT ATGGACACTC CATCAGGTGT
1543 TAAGGATTCC ATTCTGCTT      840
E--> 1545 GGATCAACTA CTCTTCACAG CTTCTGATG AAATTCCATA TAATGGAATA
1546 TATTATGATC      900
E--> 1548 CACCCGAAGA GGAGAGGTAT ATCTTCCAAC ACCCACGGCC
1549 AAAGAAACCA AAGTCGCTGA      960
E--> 1551 GAATATATGA ATCTCATATT GGAATGAGTA GTCCGGAGCC TAAAATTAAC
1552 TCATACGTGA      1020
E--> 1554 ATTTTAGAGA TGAAGTTCTT CCTCGCATAA AAAAGCTTGG GTACAATGCG
1555 GTGCAAATTA      1080
E--> 1557 TGGCTATTCA AGAGCATTCT TATTATGCTA GTTTTGGTTA TCATGTCACA
1558 AATTTTTTTG      1140
E--> 1560 CACCAAGCAG CCGTTTTTGA ACGCCCGACG ACCTTAAGTC TTTGATTGAT
1561 AAAGCTCATG      1200
E--> 1563 AGCTAGGAAT TGTGTGTTCT ATGGACATTG TTCACAGCCA TGCATCAAAT
1564 AATACTTTAG      1260
E--> 1566 ATGGACTGAA CATGTTTGGC GGCACCGATA GTTGTTACTT TCACTCTGGA
1567 GCTCGTGGTT      1320
E--> 1569 ATCATTGGAT GTGGGATTCC CGCCTTTTTA ACTATGGAAA CTGGGAGGTA
1570 CTTAGGTATC      1380
E--> 1572 TTCTCTCAAA TGCGAGATGG TGGTTGGATG AGTTCAAATT TGATGGATTT
1573 AGATTTGATG      1440
E--> 1575 GTGTGACATC AATGATGTAT ACTACCACG GATTATCGGT GGGATTCACT
1576 GGGAACTACG      1500
E--> 1578 AGGAATACTT TGGACTCGCA ACTGATGTGG ATGCTGTTGT GTATCTGATG
1579 CTGGTCAACG      1560
E--> 1581 ATCTTATTCA TGGGCTTTTC CCAGATGCAA TTACCATTGG TGAAGATGTT
1582 AGCGGAATGC      1620
E--> 1584 CGACATTTT TATTCCCGTT CAAGATGGGG GTGTGGCTT TGAATATCGG
1585 CTGCATATGG      1680
E--> 1587 CAATTGCTGA TAAATGGATT GAGTTGCTCA AGAAACGGGA TGAGGATTGG
1588 AGAGTGGGTG      1740
E--> 1590 ATATTGTTCA TACACTGACA AATAGAAGAT GGTGCGAAAA GTGTGTTTCA
1591 TACGCTGAAA      1800
E--> 1593 GTCATGATCA AGCTCTAGTC GGTGATAAAA CTATAGCATT CTGGCTGATG
1594 GACAAGGATA      1860
E--> 1596 TGTATGATTT TATGGCTCTG GATAGACCGC CAACATCATT AATAGATCGT
1597 GGGATAGCAT      1920
E--> 1599 TGCACAAGAT GATTAGGCTT GTAACATGG GATTAGGAGG
1600 AGAAGGGTAC CTAAATTTCA      1980
E--> 1602 TGGGAAATGA ATTCGGCCAC CCTGAGTGGG TTGATTTCCT
1603 TAGGGCTGAA CAACACCTCT      2040
E--> 1605 CTGATGACTC AGTAATTCCC GGAAACCAAT TCAGTTATGA TAAATGCAGA
1606 CGGAGATTG      2100
E--> 1608 ACCTGGGAGA TGCAGAATAT TTAAGATACC GTGGGTTGCA AGAATTTGAC
1609 CGGGCTATGC      2160

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RAW SEQUENCE LISTING

DATE: 02/15/2002

PATENT APPLICATION: US/10/056,454

TIME: 14:39:24

Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

E--> 1611 AGTATCTTGA AGATAAATAT GAGTTTATGA CTTCAGAACA CCAGTTCATA
1612 TCACGAAAGG 2220
E--> 1614 ATGAAGGAGA TAGGATGATT GTATTTGAAA AAGGAAACCT AGTTTTTGTC
1615 TTAAATTTTC 2280
E--> 1617 ACTGGACAAA AAGCTATTCA GACTATCGCA TAGGCTGCCT
1618 GAAGCCTGGA AAATACAAGG 2340
E--> 1620 TTGCCTTGGG CTCAGATGAT CCACTTTTTG GTGGCTTCGG GAGAATTGAT
1621 CATAATGCCG 2400
E--> 1623 AATATTTCAC CTTTGAAGGA TGGTATGATG ATCGTCCTCG TTCAATTATG
1624 GTGTATGCAC 2460
E--> 1626 CTTGTAGAAC AGCAGTGGTC TATGCACTAG TAGACAAAGA AGAAGAAGAA
1627 GAAGAAGAAG 2520
E--> 1629 AAGAAGAAGT AGCAGTAGTA GAAGAAGTAG TAGTAGAAGA
1630 AGAATGAACG AACTTGTG 2578

same

10/056,454 2c

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: *↑ must be - all responses must be on same line as heading*
~~(A) NAME:~~ National Starch and Chemical Investment Holding Corporation
~~(B) STREET:~~ 501 Silverside Road, Suite 27
~~(C) CITY:~~ Wilmington
~~(D) STATE:~~ Delaware
~~(E) COUNTRY:~~ United States of America
~~(F) POSTAL CODE (ZIP):~~ 19609

Delete

(ii) TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition

(iii) NUMBER OF SEQUENCES: 20

(v) ~~(iv)~~ COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(*) CORRESPONDENCE ADDRESS:
(1) ADDRESSEE:
(2) STREET:
(3) CITY:
(4) STATE:
(5) COUNTRY:
(6) ZIP:

insert these mandatory headings and

(*) CURRENT APPLICATION DATA:
(1) APPLICATION NUMBER:
(2) FILING DATE:

responses for U.S. applications

(2) INFORMATION FOR SEQ ID NO: 1:

insert mandatory headings

EPO format is initial for U.S. applications

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/056,454

DATE: 02/15/2002

TIME: 14:39:25

Input Set : A:\EP.txt

Output Set: N:\CRF3\02152002\J056454.raw

L:13 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
 L:20 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
 L:6 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1) Value not provided
 L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)
 L:0 M:248 E: Inserted missing Mandatory Header Field, [(iv) CORRESPONDENCE ADDRESS:]
 L:0 M:247 C: Inserted Optional Header Field, [(viii) ATTORNEY/AGENT INFORMATION:]
 L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]
 L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]
 L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
 L:41 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1
 L:218 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:12
 M:254 Repeated in SeqNo=12
 L:384 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:13
 M:254 Repeated in SeqNo=13
 L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
 L:551 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:14
 M:254 Repeated in SeqNo=14
 L:833 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
 L:835 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
 L:847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
 L:1042 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:16
 M:254 Repeated in SeqNo=16
 L:1185 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:17
 M:254 Repeated in SeqNo=17
 L:1327 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:18
 M:254 Repeated in SeqNo=18
 L:1503 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:19
 M:254 Repeated in SeqNo=19